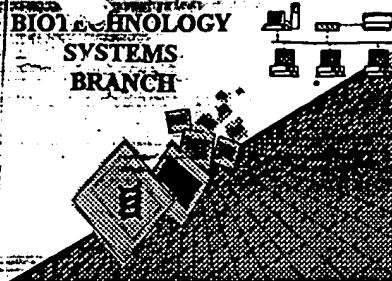


RAW SEQUENCE LISTING ERROR REPORT



2-09-01

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/737,476

Source: OIPE

Date Processed by STIC: 01-08-01

TC 3700 MAIL ROOM

JAN 24 2001

RECEIVED

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/737,476

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ☐ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ☐. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) ☐ are missing this mandatory field or its response.
- 12 ☒ Use of <220>Feature (NEW RULES) Sequence(s) 2, 5, 7 are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING

DATE: 01/08/2001

PATENT APPLICATION: US/09/737,476

TIME: 17:22:26

Input Set : A:\Frenken-seq.txt

Output Set: N:\CRF3\01082001\I737476.raw

Does Not Comply
Corrected Diskette Needed
pp 2, 3, 4

```

3 <110> APPLICANT: Unilever plc
4   Unilever NV
6 <120> TITLE OF INVENTION: Production of Antibodies
8 <130> FILE REFERENCE: T7060
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/737,476
C--> 10 <141> CURRENT FILING DATE: 2000-12-18
10 <160> NUMBER OF SEQ ID NOS: 67
12 <170> SOFTWARE: PatentIn version 3.0
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 440
16 <212> TYPE: DNA
17 <213> ORGANISM: Artificial
19 <220> FEATURE:
20 <223> OTHER INFORMATION: VHH with peptide linker
22 <220> FEATURE:
23 <221> NAME/KEY: CDS
24 <222> LOCATION: (1)..(417)
26 <400> SEQUENCE: 1
27 cag gtg cag ctg cag gag tca ggg gga gga ttg gtg cag gct ggg ggc      48
28 Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
29 1          5          10          15
31 tct ctg aga ctc tcc tgt gca gcc tgg gga cgc gcc acc agt ggt cat      96
32 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser Gly His
33          20          25          30
35 ggt cac tat ggt atg ggc tgg ttc cgc cag gtt cca ggg aag gag cgt      144
36 Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys Glu Arg
37          35          40          45
39 gag ttt gtc gca gct att agg tgg agt ggt aaa gag aca tgg tat aaa      192
40 Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp Tyr Lys
41          50          55          60
43 gac tcc gtg aag ggc cga ttc acc atc tcc aga gat aac gcc aag act      240
44 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr
45 65          70          75          80
47 acg gtt tat ctg caa atg aac agc ctg aaa cct gaa gat acg gcc gtt      288
48 Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val
49          85          90          95
51 tat tat tgt gcc gct cga ccg gtc cgc gtg gat gat att tcc ctg ccg      336
52 Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu Pro
53          100          105          110
55 gtt ggg ttt gac tac tgg ggc cag ggg acc cag gtc acc gtc tcc tca      384
56 Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
57          115          120          125
59 gaa caa aaa ctc atc tca gaa gag gat ctg aat taataagggc taagctcgaa      437
60 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
61          130          135
63 ttc      440
66 <210> SEQ ID NO: 2

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RAW SEQUENCE LISTING DATE: 01/08/2001
 PATENT APPLICATION: US/09/737,476 TIME: 17:22:26

Input Set : A:\Frenken-seq.txt
 Output Set: N:\CRF3\01082001\I737476.raw

67 <211> LENGTH: 139
 68 <212> TYPE: PRT
 69 <213> ORGANISM: Artificial
 71 <400> SEQUENCE: 2
 73 Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 74 1 5 10 15
 77 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Ala Thr Ser Gly His
 78 20 25 30
 81 Gly His Tyr Gly Met Gly Trp Phe Arg Gln Val Pro Gly Lys Glu Arg
 82 35 40 45
 85 Glu Phe Val Ala Ala Ile Arg Trp Ser Gly Lys Glu Thr Trp Tyr Lys
 86 50 55 60
 89 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Thr
 90 65 70 75 80
 93 Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val
 94 85 90 95
 97 Tyr Tyr Cys Ala Ala Arg Pro Val Arg Val Asp Asp Ile Ser Leu Pro
 98 100 105 110
 101 Val Gly Phe Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
 102 115 120 125
 105 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
 106 130 135
 109 <210> SEQ ID NO: 3
 110 <211> LENGTH: 11
 111 <212> TYPE: PRT
 112 <213> ORGANISM: Artificial
 114 <220> FEATURE:
 115 <223> OTHER INFORMATION: myc linker
 117 <400> SEQUENCE: 3
 119 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn
 120 1 5 10
 122 <210> SEQ ID NO: 4
 123 <211> LENGTH: 471
 124 <212> TYPE: DNA
 125 <213> ORGANISM: Artificial
 127 <220> FEATURE:
 128 <223> OTHER INFORMATION: VHH with linker
 130 <220> FEATURE:
 131 <221> NAME/KEY: CDS
 132 <222> LOCATION: (1)..(459)
 134 <400> SEQUENCE: 4
 135 Cag gtg cag ctg cag cag tca ggg gga ggc ttg gtg cag gct ggg ggg 48
 136 Gln Val Gln Leu Gln Gln Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
 137 1 5 10 15
 139 tct ctg aga ctc tcc tgt gta gct tct gaa agc agc ttc agc aac aat 96
 140 Ser Leu Arg Leu Ser Cys Val Ala Ser Glu Ser Ser Phe Ser Asn Asn
 141 20 25 30
 143 cac atg ggc tgg tac cgc cgg gct cca ggg aac cag cgc gag ctg gtc 144
 144 His Met Gly Trp Tyr Arg Arg Ala Pro Gly Asn Gln Arg Glu Leu Val

*missing mandatory <220>, <223> features
 to explain artificial sequence. See
 #12 on Error
 Summary sheet.*

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/737,476
 DATE: 01/08/2001
 TIME: 17:22:26

Input Set : A:\Frenken-seq.txt
 Output Set: N:\CRF3\01082001\I737476.raw

```

145      35      40      45
147 gca act att agt cct ggt ggt agc aca cac tat gta gac tcc gtg aag 192
148 Ala Thr Ile Ser Pro Gly Gly Ser Thr His Tyr Val Asp Ser Val Lys
149      50      55      60
151 ggc cga ttc acc atc tcc cga gac aac gcc aag aac aca gtg tat cta 240
152 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
153 65      70      75      80
155 caa atg gac agc ctg aaa cca gag gac acg gcc gtc tat tac tgt gct 288
156 Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
157      85      90      95
159 gcc aag ggg agg ggg ctg cag gct atg cag tac tgg ggc cag ggg acc 336
160 Ala Lys Gly Arg Gly Leu Gln Ala Met Gln Tyr Trp Gly Gln Gly Thr
161      100      105      110
163 ctg gtc acc gtc tcc tca gcg cac cac agc gaa gac ccc agc tcc gcg 384
164 Leu Val Thr Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala
165      115      120      125
167 gcc gcc cat cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc 432
168 Ala Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile
169      130      135      140
171 tca gaa gag gat ctg aat ggg gcc gca tagtaacaat tg 471
W--> 172 Ser Glu Glu Asp Leu Asn Gly Ala Ala
173 145      150
176 <210> SEQ ID NO: 5
177 <211> LENGTH: 153
178 <212> TYPE: PRT
179 <213> ORGANISM: Artificial
181 <400> SEQUENCE: 5
183 Gln Val Gln Leu Gln Gln Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
184 1      5      10      15
187 Ser Leu Arg Leu Ser Cys Val Ala Ser Glu Ser Ser Phe Ser Asn Asn
188      20      25      30
191 His Met Gly Trp Tyr Arg Arg Ala Pro Gly Asn Gln Arg Glu Leu Val
192      35      40      45
195 Ala Thr Ile Ser Pro Gly Gly Ser Thr His Tyr Val Asp Ser Val Lys
196      50      55      60
199 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
200 65      70      75      80
203 Gln Met Asp Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
204      85      90      95
207 Ala Lys Gly Arg Gly Leu Gln Ala Met Gln Tyr Trp Gly Gln Gly Thr
208      100      105      110
211 Leu Val Thr Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala
212      115      120      125
215 Ala Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile
216      130      135      140
219 Ser Glu Glu Asp Leu Asn Gly Ala Ala
220 145      150
223 <210> SEQ ID NO: 6
224 <211> LENGTH: 468

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*Missing <220>, <223>
See #12*

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/737,476
 DATE: 01/08/2001
 TIME: 17:22:27

Input Set : A:\Frenken-seq.txt
 Output Set: N:\CRF3\01082001\I737476.raw

```

225 <212> TYPE: DNA
226 <213> ORGANISM: Artificial
228 <220> FEATURE:
229 <223> OTHER INFORMATION: VHH with linker
231 <220> FEATURE:
232 <221> NAME/KEY: CDS
233 <222> LOCATION: (1)..(456)
235 <400> SEQUENCE: 6
236 'cag gtg cag ctg cag gag tct ggg gga ggc ctg gtg cag gct ggg ggg      48
237 Gln Val Gln Leu Gln Glu Ser Gly Gly Leu Val Gln Ala Gly Gly
238 1          5          10          15
240 tct ctg aga ctc tcc tgt gta gcc tct gga aac acc ttc agt atc ata      96
241 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Asn Thr Phe Ser Ile Ile
242          20          25          30
244 gct atg gcc tgg tac cgc cag gct cca ggg aaq cag cgc gag gtg gtc      144
245 Ala Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Val Val
246          35          40          45
248 gca agt att aat agt att ggc agc aca aat tat gca gac tcc gtg aag      192
249 Ala Ser Ile Asn Ser Ile Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys
250          50          55          60
252 ggg cga ttc acc atc tcc aga gac aac gcc aag aac aca gtg tat ctg      240
253 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
254 65          70          75          80
256 caa atg agc agc ctg aaa cct gag gac acg gcc gtc tat tac tgt gct      288
257 Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
258          85          90          95
260 gcc ggt aat ttg ctg gtt aag agg cct tac tgg ggc cag ggg acc ctg      336
261 Ala Gly Asn Leu Leu Val Lys Arg Pro Tyr Trp Gly Gln Gly Thr Leu
262          100          105          110
264 gtc acc gtc tcc tca gaa ccc aag aca cca aaa cca caa cca gcg gcc      384
265 Val Thr Val Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala
266          115          120          125
268 gcc cat cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca      432
269 Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser
270          130          135          140
272 gaa gag gat ctg aat ggg gcc gca tagtaacaat tg      468
W--> 273 Glu Glu Asp Leu Asn Gly Ala Ala
274 145          150
277 <210> SEQ ID NO: 7
278 <211> LENGTH: 152
279 <212> TYPE: PRT
280 <213> ORGANISM: Artificial
282 <400> SEQUENCE: 7
284 Gln Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
285 1          5          10          15
288 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Asn Thr Phe Ser Ile Ile
289          20          25          30
292 Ala Met Ala Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Val Val
293          35          40          45

```

*Missing <220>, <223>
 See #12*

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/737,476
 DATE: 01/08/2001
 TIME: 17:22:27

Input Set : A:\Frenken-seq.txt
 Output Set: N:\CRF3\01082001\I737476.raw

```

296 Ala Ser Ile Asn Ser Ile Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys
297      50      55      60
300 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
301 65      70      75      80
304 Gln Met Ser Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
305      85      90      95
308 Ala Gly Asn Leu Leu Val Lys Arg Pro Tyr Trp Gly Gln Gly Thr Leu
309      100     105     110
312 Val Thr Val Ser Ser Glu Pro Lys Thr Pro Lys Pro Gln Pro Ala Ala
313      115     120     125
316 Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu Ile Ser
317      130     135     140
320 Glu Glu Asp Leu Asn Gly Ala Ala
321 145     150
324 <210> SEQ ID NO: 8
325 <211> LENGTH: 462
326 <212> TYPE: DNA
327 <213> ORGANISM: Artificial
329 <220> FEATURE:
330 <223> OTHER INFORMATION: VHH with linker
332 <220> FEATURE:
333 <221> NAME/KEY: CDS
334 <222> LOCATION: (1)..(450)
336 <400> SEQUENCE: 8
337 acc atg gcc cag gtg aaa ctg cag cag tct ggg gga gga ttg gtg cag      48
338 Thr Met Ala Gln Val Lys Leu Gln Gln Ser Gly Gly Gly Leu Val Gln
339 1      5      10      15
341 gct ggg ggc cct ctg agg ctc tcc tgt gca gcc tct gga cgc acc ttc      96
342 Ala Gly Gly Pro Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Phe
343      20      25      30
345 agt aac tat gcc gtg ggc tgg ttc cgc cag gct cca ggg aag gag cgt      144
346 Ser Asn Tyr Ala Val Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg
347      35      40      45
349 gag ttt gtc gct gct att agc cgt gat ggt ggg cgc aca tac tat gcg      192
350 Glu Phe Val Ala Ala Ile Ser Arg Asp Gly Gly Arg Thr Tyr Tyr Ala
351      50      55      60
353 gac tcc gtg aag ggc cga ttc gcc gtc tcc aga gac tac gcc gag aac      240
354 Asp Ser Val Lys Gly Arg Phe Ala Val Ser Arg Asp Tyr Ala Glu Asn
355 65      70      75      80
357 acg gtg tat ctg caa atg aac agc ctg aaa cct gag gac acg gcc gtt      288
358 Thr Val Tyr Leu Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val
359      85      90      95
361 tat tac tgt aac aca agg gcc tac tgg ggc cag ggg acc cag gtc acc      336
362 Tyr Tyr Cys Asn Thr Arg Ala Tyr Trp Gly Gln Gly Thr Gln Val Thr
363      100     105     110
365 gtc tcc tca gcg cac cac agc gaa gac ccc agc tcc gcg gcc gcc cat      384
366 Val Ser Ser Ala His His Ser Glu Asp Pro Ser Ser Ala Ala Ala His
367      115     120     125
369 cac cat cac cat cac ggg gcc gca gaa caa aaa ctc atc tca gaa gag      432

```

VERIFICATION SUMMARY DATE: 01/08/2001
PATENT APPLICATION: US/09/737,476 TIME: 17:22:28

Input Set : A:\Frenken-seq.txt
Output Set: N:\CRF3\01082001\I737476.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:172 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 4
L:273 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 6
L:374 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 8
L:475 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 10
L:1684 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 66